

1683

P#20



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/469,200D

DATE: 11/18/2002

TIME: 13:01:24

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RECEIVED

NOV 29 2002

TECH CENTER 1600/2900

3 <110> APPLICANT: Weigel, Paul H.
4 DeAngelis, Paul
5 Kumari, Kshama
7 <120> TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
9 <130> FILE REFERENCE: 3554.011
11 <140> CURRENT APPLICATION NUMBER: US 09/469,200D
12 <141> CURRENT FILING DATE: 1999-12-21
14 <150> PRIOR APPLICATION NUMBER: US 09/178,851
15 <151> PRIOR FILING DATE: 1998-10-26
17 <150> PRIOR APPLICATION NUMBER: US 60/064,435
18 <151> PRIOR FILING DATE: 1997-10-31
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1254
26 <212> TYPE: DNA
27 <213> ORGANISM: Streptococcus equisimilis
29 <400> SEQUENCE: 1

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34 ctgatatgctt acctattagt caaaatgtcc ttatcctttt ttacaagcc atttaaggga	180
36 agggctgggc aatataaggt tgcagccatt attcctctt ataacgaaga tgctgagtca	240
38 ttgctagaga ccttaaaaag tgttcagcag caaacctatc ccctagcaga aatttatggt	300
40 gttgacgatg gaagtgtgta tgagacaggt attaagcgca ttgaagacta tgtgcgtgac	360
42 actggtgacc tatcaagcaa tgtcattggt catcggtcag agaaaaatca aggaaagcgt	420
44 catgcacagg cctgggcctt tgaaagatca gacgctgatg tctttttgac cgttgactca	480
46 gatacttata tctaccctga tgcctttagag gagttgttaa aaaccttta tgaccaact	540
48 gtttttgcgt cgacgggtca ccttaatgtc agaaatagac aaaccaatct cttaacacgc	600
50 ttgacagata ttcgctatga taatgctttt ggcgttgaa gagctgcca atccgttaca	660
52 ggtaatatcc ttgtttgctc aggtccgctt agcgtttaca gacgagagg ggtgttcct	720
54 aacatagata gatacatcaa ccagaccttc ctgggtattc ctgtaagtat tggatgatgac	780
56 aggtgcttga ccaactatgc aactgattta ggaaagactg tttatcaatc cactgctaaa	840
58 tgtattacag atgttcctga caagatgtct acttacttga agcagcaaaa ccgctggaac	900
60 aagtccttct ttagagagtc cattatttct gttaaagaaa tcatgaacaa tccttttgta	960
62 gccctatgga ccatacttga ggtgtctatg tttatgatgc ttgtttatc tgtggtggat	1020
64 ttcttttgtag gcaatgtcag agaatttgat tggctcagg ttttagcctt tctggtgatt	1080
66 atcttcattg ttgccctgtg tcggaacatt cattacatgc ttaagcacc gctgtccttc	1140
68 ttgttatctc cgttttatgg ggtgctgcac ttgtttgtcc tacagccctt gaaattatat	1200
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74 <211> LENGTH: 417
75 <212> TYPE: PRT
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80 Met Arg Thr Leu Lys Asn Leu Ile Thr Val Val Ala Phe Ser Ile Phe
81 1 5 10 15
84 Trp Val Leu Leu Ile Tyr Val Asn Val Tyr Leu Phe Gly Ala Lys Gly
85 20 25 30
88 Ser Leu Ser Ile Tyr Gly Phe Leu Leu Ile Ala Tyr Leu Leu Val Lys
89 35 40 45
92 Met Ser Leu Ser Phe Phe Tyr Lys Pro Phe Lys Gly Arg Ala Gly Gln
93 50 55 60
96 Tyr Lys Val Ala Ala Ile Ile Pro Ser Tyr Asn Glu Asp Ala Glu Ser
97 65 70 75 80
100 Leu Leu Glu Thr Leu Lys Ser Val Gln Gln Gln Thr Tyr Pro Leu Ala
101 85 90 95
104 Glu Ile Tyr Val Val Asp Asp Gly Ser Ala Asp Glu Thr Gly Ile Lys
105 100 105 110
108 Arg Ile Glu Asp Tyr Val Arg Asp Thr Gly Asp Leu Ser Ser Asn Val
109 115 120 125
112 Ile Val His Arg Ser Glu Lys Asn Gln Gly Lys Arg His Ala Gln Ala
113 130 135 140
116 Trp Ala Phe Glu Arg Ser Asp Ala Asp Val Phe Leu Thr Val Asp Ser
117 145 150 155 160
120 Asp Thr Tyr Ile Tyr Pro Asp Ala Leu Glu Glu Leu Leu Lys Thr Phe
121 165 170 175
124 Asn Asp Pro Thr Val Phe Ala Ala Thr Gly His Leu Asn Val Arg Asn
125 180 185 190
128 Arg Gln Thr Asn Leu Leu Thr Arg Leu Thr Asp Ile Arg Tyr Asp Asn
129 195 200 205
132 Ala Phe Gly Val Glu Arg Ala Ala Gln Ser Val Thr Gly Asn Ile Leu
133 210 215 220
136 Val Cys Ser Gly Pro Leu Ser Val Tyr Arg Arg Glu Val Val Val Pro
137 225 230 235 240
140 Asn Ile Asp Arg Tyr Ile Asn Gln Thr Phe Leu Gly Ile Pro Val Ser
141 245 250 255
144 Ile Gly Asp Asp Arg Cys Leu Thr Asn Tyr Ala Thr Asp Leu Gly Lys
145 260 265 270
148 Thr Val Tyr Gln Ser Thr Ala Lys Cys Ile Thr Asp Val Pro Asp Lys
149 275 280 285
152 Met Ser Thr Tyr Leu Lys Gln Gln Asn Arg Trp Asn Lys Ser Phe Phe
153 290 295 300
156 Arg Glu Ser Ile Ile Ser Val Lys Lys Ile Met Asn Asn Pro Phe Val
157 305 310 315 320
160 Ala Leu Trp Thr Ile Leu Glu Val Ser Met Phe Met Met Leu Val Tyr
161 325 330 335
164 Ser Val Val Asp Phe Phe Val Gly Asn Val Arg Glu Phe Asp Trp Leu
165 340 345 350
168 Arg Val Leu Ala Phe Leu Val Ile Ile Phe Ile Val Ala Leu Cys Arg
169 355 360 365
172 Asn Ile His Tyr Met Leu Lys His Pro Leu Ser Phe Leu Leu Ser Pro
173 370 375 380

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176 Phe Tyr Gly Val Leu His Leu Phe Val Leu Gln Pro Leu Lys Leu Tyr
177 385                      390                      395                      400
180 Ser Leu Phe Thr Ile Arg Asn Ala Asp Trp Gly Thr Arg Lys Lys Leu
181                      405                      410                      415
184 Leu
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189 <211> LENGTH: 22
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Primer sel
196 <400> SEQUENCE: 3
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201 <211> LENGTH: 20
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Primer se2
208 <400> SEQUENCE: 4
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213 <211> LENGTH: 20
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Primer sespl
220 <400> SEQUENCE: 5
221 gactcagata cttatatcta                                20
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225 <211> LENGTH: 17
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Primer sesp2
232 <400> SEQUENCE: 6
233 tttttacgtg ttcccca                                17
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 1740
238 <212> TYPE: DNA
239 <213> ORGANISM: Paramecium bursaria chlorella virus
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244 tcataacttc aaatctaadc gcggttgagg gagcctctct aatcttggct ccggcaatta    120
246 ctgggtatgt tctacattgg aatattgctc tctcgacaat ctggggagta tcagcttatg    180
248 gtattttcgt ttttgggttt ttccttgcaac aagttttatt ttcagaactg aacaggaaac    240
250 gtcttcgcaa gtggatttct ctcagacctc aggggttgaa tgatgttcgt ttggctgtga    300
252 tcattgctgg atatcgcgag gatccttata tgttcagaa gtgcctcgag tctgtacgtg    360
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258 ttgttctgtg tgagtcagac gacaaggaa gtgaacgcat cgactctgat ttctctcgcg 540
260 acatttgtgt cctccagcct catcgtggaa aacgggagtg tctttatact gggtttcaac 600
262 ttgcaaagat ggaccccagt gtcaatgctg tcgttctgat tgacagcgat accgttctcg 660
264 agaaggatgc tattctggaa gttgtatacc cacttgcatg cgatcccag atccaagccg 720
266 ttgcaggatga gtgtaagatt tggaacacag aactctttt gagtcttctc gtcgcttggc 780
268 ggtactattc tgcgttttgt gtggagagga gtgccagtc ttttttcagg actgttcagt 840
270 gcgttggggg gccactgggt gcctacaaga ttgatatcat taaggagatt aaggaccct 900
272 ggatttccca gcgctttctt ggtcagaagt gtacttacgg tgacgaccgc cggctaacca 960
274 acgagatctt gatgcgtggt aaaaagggtt gtgtcactcc atttgctggt ggttggtctg 1020
276 acagtcggac caatgtgttt cggtagatcg ttacgcagac ccgctggagt aagtcgtggt 1080
278 gccgcgaaat ttggtacacc ctcttcgcgc cgtggaagca cggtttgtct ggaatttggc 1140
280 tggcctttga atgtttgtat caaattacat acttcttctt cgtgatttac ctcttttctc 1200
282 gcctagccgt tgaggccgac cctcgcgcgc agacagccac ggtgattgtg agcaccacgg 1260
284 ttgcattgat taagtgtggg ttttttcat tccgagccaa ggatattcgg gcgttttact 1320
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288 tgacgctttg ggacattggc tggggtactc gcgttgaaaa cgagaagcct tccgttggca 1440
290 cccgggtcgc tctgtgggca aagcaatata tcattgcata tatgtggtgg gccgcggtt 1500
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296 tttatttcac cggcaaaatt acgacttgga atttcacgaa gcttcagaag gagctaactg 1680
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302 <211> LENGTH: 2937
303 <212> TYPE: DNA
304 <213> ORGANISM: Pastuerella Multocida
306 <400> SEQUENCE: 8
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311 gttgaatttc aaattaccaa atgcaaagaa aaactctcag cacatccttc tgttaattca 180
313 gcacatcttt ctgtaaataa agaagaaaaa gtcaatgttt gcgatagtc gttagatatt 240
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317 acgttaaaaa ataaatggaa attgtcact gagaagaaat ctgaaaatgc ggaggttaaga 360
319 gcggtcgcgc ttgtaccaa agattttccc aaagatctgg ttttagcgcc ttacctgat 420
321 catgttaatg attttacctg gtacaaaaag cgaaagaaaa gacttggcat aaaacctgaa 480
323 catcaacatg ttggtctttc tattatcggt acaacattca atcgaccagc aattttatcg 540
325 attacattag cctgttttagt aaaccaaaaa acacattacc cgtttgaagt tatcgtgaca 600
327 gatgatggta gtcaggaaga tctatcaccg atcattcgcc aatatgaaaa taaattggat 660
329 attcgctacg tcagacaaaa agataacggg tttcaagcca gtgccgctcg gaatatggga 720
331 ttacgcttag caaaatatga ctttattggc ttactcgact gtgatatggc gccaaatcca 780
333 ttatgggttc attcttatgt tgcagagcta ttagaagatg atgatttaac aatcattggt 840
335 ccaagaaaat acatcgatac acaacatatt gacccaaaaag acttcttaaa taacgcgagt 900
337 ttgcttgaat cattaccaga agtgaaaacc aataatagtg ttgocgcaaa aggggaagga 960
339 acagtttctc tggattggcg cttagaacaa ttcgaaaaaa cagaaaatct ccgcttatcc 1020
341 gattcgctt tccgtttttt tgcggcgggt aatgttgcct tcgctaaaaa atggctaaat 1080
343 aaatccgggt tctttgatga ggaatttaat cactggggtg gagaagatgt ggaatttggg 1140
345 tatcgcttat tccgttacgg tagtttcttt aaaactattg atggcattat ggcctaccat 1200
347 caagagccac caggtaaaga aaatgaaacc gatcgtgaag cgggaaaaaa tattacgctc 1260
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355 tgtaacgatg gttcaacaga taatacctta gaagtgatca ataagcttta tggtataaat 1500
357 cctaggggtac gcatcatgtc taaaccaaatt ggcggaatag cctcagcatc aaatgcagcc 1560
359 gtttcttttg ctaaagggtta ttacattggg cagtttagatt cagatgatta tcttgagcct 1620
361 gatgcagttg aactgtgttt aaaagaattt ttaaaagata aaacgctagc ttgtgtttat 1680
363 accactaata gaaacgtcaa tccggatggt agcttaatcg ctaatgggta caattggcca 1740
365 gaattttcac gagaaaaact cacaacggct atgattgctc accactttag aatgttcacg 1800
367 attagagctt ggcatttaac tgatggattc aatgaaaaaa ttgaaaatgc cgtagactat 1860
369 gacatgttcc tcaaactcag tgaagttgga aaattttaa acatctgctat 1920
371 aaccgtgtat tacatgggtga taacacatca attaagaaac ttggcattca aaagaaaaac 1980
373 cattttgttg tagtcaatca gtcattaaat agacaaggca taacttatta taattatgac 2040
375 gaatttgatg atttagatga aagtagaaaag tatattttca ataaaaccgc tgaatatcaa 2100
377 gaagagattg atatcttaaa agatattaaa atcatccaga ataaagatgc caaaatcgca 2160
379 gtcagtattt tttatcccaa tacattaaac ggcttagtga aaaaactaaa caatattatt 2220
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397 atcacatctt gccagtcaat tgatagtgtg ccagaatata aactgagga tatttggttc 2760
399 caatttgcac ttttaattct agaaaaagaaa accggccatg tatttaataa aacatcgacc 2820
401 ctgacttata tgccttgga acgaaaatta caatggacaa atgaacaaat tgaaagtgc 2880
403 aaaagaggag aaaatatacc tgtaacaag ttcattatta atagtataac tctataa 2937

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406 <210> SEQ ID NO: 9

407 <211> LENGTH: 972

408 <212> TYPE: PRT

409 <213> ORGANISM: *Pastuerella Multocida*

411 <400> SEQUENCE: 9

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414 1 5 10 15
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418 20 25 30
421 Lys Ile Val Glu Phe Gln Ile Thr Lys Cys Lys Glu Lys Leu Ser Ala
422 35 40 45
425 His Pro Ser Val Asn Ser Ala His Leu Ser Val Asn Lys Glu Glu Lys
426 50 55 60
429 Val Asn Val Cys Asp Ser Pro Leu Asp Ile Ala Thr Gln Leu Leu Leu
430 65 70 75 80
433 Ser Asn Val Lys Lys Leu Val Leu Ser Asp Ser Glu Lys Asn Thr Leu
434 85 90 95
437 Lys Asn Lys Trp Lys Leu Leu Thr Glu Lys Lys Ser Glu Asn Ala Glu
438 100 105 110
441 Val Arg Ala Val Ala Leu Val Pro Lys Asp Phe Pro Lys Asp Leu Val
442 115 120 125
445 Leu Ala Pro Leu Pro Asp His Val Asn Asp Phe Thr Trp Tyr Lys Lys

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VERIFICATION SUMMARY

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